

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
ROBERTS-RAPP, LISA
RUSSELL, JOHN C.
STROUPE, STEPHEN D.

(ii) TITLE OF THE INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE PROSTATE

(iii) NUMBER OF SEQUENCES: 41

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Abbott Laboratories
(B) STREET: 100 Abbott Park Road
(C) CITY: Abbott Park
(D) STATE: IL
(E) COUNTRY: USA
(F) ZIP: 60064-3500

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/850,713
(B) FILING DATE: 02-MAY-1997

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Becker, Cheryl L.
(B) REGISTRATION NUMBER: 35,441
(C) REFERENCE/DOCKET NUMBER: 6083.US.P1

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 847/935-1729
(B) TELEFAX: 847/938-2623
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGGGCTGTAC CAGGGCGTGC CCAGAGCTGA GCCGGGCACC GAGGCCCGGA GACACTATGA	60
TGAAGGCAGTT CGGATGGGCA GCCTGGGGCT GTTCCTGCAG TGCGCCATCT CCCTGGTCTT	120
CTCTCTGGTC ATGGACCGGC TGGTGCAGCG ATTGGCAGT CTGGCAGTCT ATTGGCCAG	180
TGTGGCAGCT TTCCCTGTGG CTGCCGGTGC CACATGCCTG TCCCACAGTG TGGCCGTGGT	240
GACAGCTTCA GCCGCCTT	258

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ACCAGGGCGT GCCCAGAGCT GAGCCGGGCA CCGAGGCCCG GAGACACTAT GATGAAGGCG	60
TTCGGATGGG CAGCCTGGGG CTGTTCTGC AGTGCAGCCAT CTCCCTGGTC TTCTCTCTGG	120
TCATGGACCG GCTGGTGCAG CGATTGGCA CTCGAGCAGT CTATTTGGCC AGTGTGGCAG	180
CTTCCCTGT GGCTGCCGGT GCCACATGCC TGTCCA	217

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: base_polymorphism
- (B) LOCATION: 215
- (D) OTHER INFORMATION: /note= "N represents an A or G or T or C polymorphism at this position"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GACAGCTTCA GCCGCCCTCA CCGGGTTCAC CTTCTCAGCC CTGCAGATCC TGCCCTACAC	60
ACTGGCCTCC CTCTACCACC GGGAGAAGCA GGTGTTCTG CCCAAATACC GAGGGGACAC	120
TGGAGGTGCT AGCAGTGAGG ACAGCCTGAT GACCAGCTTC CTGCCAGGCC CTAAGCCTGG	180
AGCTCCCTTC CCTAATGGAC ACGTGGGTGC TGGANGCAGT GGCCTGCTCC CACCTCCACC	240
CGCGCTCTGC GGGGC	255

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCTCCCTTCC CTAATGGACA CGTGGGTGCT GGAGGCAGTG GCCTGCTCCC ACCTCCACCC	60
GCGCTCTGCG GGGCCTCTGC CTGTGATGTC TCCGTACGTG TGGTGGTGGG TGAGCCCACC	120
GAGGCCAGGG TGGTTCCGGG CCGGGGCATC TGCCTGGACC TCGCCATCCT GGATAGTGCC	180
TTCCTGCTGT CCCAGGTGGC CCCATCCCTG TTTATGGGCT CCATTGTCCA GCTCAGGCCAG	240
TCTGTCA	247

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TGGATAGTGC CTTCCTGCTG TCCCAGGTGG CCCCATCCCT GTTTATGGGC TCCATTGTCC	60
AGCTCAGCCA GTCTGTCACT GCCTATATGG TGTCTGCCGC AGGCTGGTC TGGTCGCCAT	120
TTACTTTGCT ACACAGGTAG TATTGACAA GAGCGACTTG GCCAAATACT CAGCGTAGAA	180
AACTTCCAGC ACATTGGGGT GGAGGGCCTG CCTCACTGGG TCCCAGCTCC C	231

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: base_polymorphism
- (B) LOCATION: 178
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CTTGGCCAAA TACTCAGCGT AGAAAACCTTC CAGCACATTG GGGTGGAGGG CCTGCCTCAC	60
TGGGTCCCAG CTCCCCGCTC CTGTTAGCCC CATGGGGCTG CGGGCTGGC CGCCAGTTTC	120
TGTTGCTGCC AAAGTAATGT GGCTCTCTGC TGCCACCCTG TGCTGCTGAG GTGCGTANTG	180
CACAGCTGGG GGCTG	195

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: base_polymorphism
- (B) LOCATION: 67
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(ix) FEATURE:

- (A) NAME/KEY: base_polymorphism
- (B) LOCATION: 222
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCCAGTTCT GTTGCTGCCA AAGTAATGTG GCTCTCTGCT GCCACCCTGT GCTGCTGAGG	60
--	----

TGGTANTGC ACAGCTGGGG GCTGGGGCGT CCCTCTCCTC TCTCCCCAGT CTCTAGGGCT	120
GCTGACTGG AGGCCTTCCA AGGGGGTTTC AGTCTGGACT TATACAGGGA GGCCAGAAGG	180
GCTCCATGCA CTGGAATGCG GGGACTCTGC AGGTGGATTA CNC	223

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: base_polymorphism
- (B) LOCATION: 323
- (D) OTHER INFORMATION: /note= "N' represents an A or G or T or C polymorphism at this position"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCCAGAAGGG CTCCATGCAC TGGAATGCGG GGACTCTGCA GGTGGATTAC CCAGGCTCAG	60
GGTTAACAGC TAGCCTCCTA GTTGAGACAC ACCTAGAGAA GGGTTTTGG GAGCTGAATA	120
AACTCAGTCA CCTGGTTTCC CATCTCTAAG CCCCTTAACC TGCAGCTTCG TTTAATGTAG	180
CTCTTGCATG GGAGTTCTA GGATGAAACA CTCCTCCATG GGATTTGAAC ATATGAAAGT	240
TATTTGTAGG GGAAGAGTCC TGAGGGGCAA CACACAAGAA CCAGGTCCCC TCAGCCCACA	300
GCACGTCTT TTTGCTGATC CANCCCCCTC TTACTTTAT CA	342

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGGGAAGAGT CCTGAGGGGC AACACACAAG AACCAGGTCC CCTCAGCCCA CAGCACTGTC	60
TTTTTGCTGA TCCACCCCCC TCTTACCTTT TATCAGGATG TGGCCTGTTG GTCCTTCTGT	120
TGCCATCACA GAGACACAGG CATTAAATA TTTAACTTAT TTATTTAACAA AAGTAGAAGG	180
GAATCCATTG CTAGCTTTTC TGTGTTGGTG TCTAATATTG GGGTAGGGTG GGGGATCCCC	240
AACAATCAGG TCCCCTGAGA TAGCT	265

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: base_polymorphism
- (B) LOCATION: 147
- (D) OTHER INFORMATION: /note= "N' represents an A or G or T or C polymorphism at this position"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CTCTTACCTT TTATCAGGAT GTGGCCTGTT GGTCCCTCTG TTGCCATCAC AGAGACACAG	60
GCATTTAAAT ATTAACTTA TTTATTAAC AAAGTAGAAG GGAATCCATT GCTAGCTTT	120
CTGTGTTGGT GTCTAATATT TGGGTANGGT GGGGGATCCC CAACAATCAG GTCCCCCTGAG	180
ATAGCTGGTC ATTGGGCTGA TCATTGCCAG AATCTTCTTC TCCTGGGTC TGGCCCCCA	240
AAATGCCTAA CCCAGGACCT TGGAAATTCT ACTCATCCCA AATGATAA	288

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: base_polymorphism
- (B) LOCATION: 216
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AAATTCTACT	CATCCCAAAT	GATAATTCCA	AATGCTGTTA	CCCAAGGTTA	GGGTGTTGAA	60
GGAAGGTAGA	GGGTGGGGCT	TCAGGTCTCA	ACGGCTTCCC	TAACCACCCC	TCTTCTCTTG	120
GCCCAGCCTG	GTTCCCCCCTA	CTTCCACTCC	CCTCTACTCT	CTCTAGGACT	GGGCTGATGA	180
AGGCACTGCC	CAAAATTCC	CCTACCCCCA	ACTTNCCT	ACCCCCAACT	TTCCCCACCA	240
GCTCCACAAAC	CCTGTTGGA	GCTACTGCAG	GT			272

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: base_polymorphism
- (B) LOCATION: 18
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(ix) FEATURE:

- (A) NAME/KEY: base_polymorphism
- (B) LOCATION: 19
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(ix) FEATURE:

- (A) NAME/KEY: base_polymorphism
- (B) LOCATION: 197
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AAGGCAC TG C	CCAAAATNNC	CCCTACCCCC	AACTTTCCCC	TACCCCCAAC	TTTCCCCACC	60
AGCTCCACAA	CCCTGTTGG	AGCTACTGCA	GGACCAGAAG	CACAAAGTGC	GGTTTCCCAA	120
GCCTTGTC	ATCTCAGCCC	CCAGAGTATA	TCTGTGCTTG	GGGAATCTCA	CACAGAAACT	180
CAGGAGCACC	CCCTGCNTGA	GCTAAGGGAG	GTCTTATCTC	TCAGGGGGGG	TTAAAGTGCC	240
GTTTGCAATA	ATGTCGTCTT	ATTATTTAG	CGGGGTGAAT	ATTTTATACT	GTAA	294

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: base_polymorphism
(B) LOCATION: 113
(D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(ix) FEATURE:

(A) NAME/KEY: base_polymorphism
(B) LOCATION: 147
(D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CTCCACAAACC	CTGTTGGAG	CTACTGCAGG	ACCAGAACCA	CAAAGTGCAG	TTTCCAAGC	60
CTTGTCAT	CTCAGCCCCC	AGAGTATATC	TGTGCTTGGG	GAATCTCAC	CANAAACTCA	120
GGAGCACCCC	CTGCCTGAGC	TAAGGGNGGT	C			151

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CCCAGAGTAT	ATCTGTGCTT	GGGAAATCTC	ACACAGAAC	TCAGGAGCAC	CCCCTGCCTG	60
AGCTAAGGGA	GGTCTTATCT	CTCAGGGGGG	GTTAAGTGC	CGTTGCAAT	AATGTCGTCT	120
TATTTATTAA	GCGGGGTGAA	TATTTATAC	TGTAAGTGAG	CAATCAGAGT	ATAATGTTA	180
TGGTGACAAA	ATTAAAGGCT	TTCTTATATG	TTT			213

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2143 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ACCAAGGGCGT	GCCCAGAGCT	GAGCCGGGCA	CCGAGGCCG	GAGACACTAT	GATGAAGGCG	60
TTCGGATGGG	CAGCCTGGGG	CTGTTCTGC	AGTGCGCCAT	CTCCCTGGTC	TTCTCTCTGG	120
TCATGGACCG	GCTGGTGCAG	CGATTGGCA	CTCGAGCAGT	CTATTGGCC	AGTGTGGCAG	180
CTTTCCCTGT	GGCTGCCGGT	GCCACATGCC	TGTCCCACAG	TGTGGCCGTG	GTGACAGCCT	240
CAGCCGCCCT	CACCGGGTTC	ACCTTCTCAG	CCCTGCAGAT	CCTGCCCTAC	ACACTGGCCT	300
CCCTCTACCA	CCGGGAGAAG	CAGGTGTTCC	TGCCCAAATA	CCGAGGGGAC	ACTGGAGGTG	360
CTAGCAGTGA	GGACAGCCTG	ATGACCAGCT	TCCTGCCAGG	CCCTAACGCCT	GGAGCTCCCT	420
TCCCTAATGG	ACACGTGGGT	GCTGGAGGCA	GTGGCCTGCT	CCCACCTCCA	CCCGCGCTCT	480
GCGGGGCCCTC	TGCCTGTGAT	GTCTCCGTAC	GTGTGGTGGT	GGGTGAGGCC	ACCGAGGCCA	540
GGGTGGTTCC	GGGCCGGGGC	ATCTGCCTGG	ACCTCGCCAT	CCTGGATAGT	GCCTTCCTGC	600
TGTCCCAGGT	GGCCCCATCC	CTGTTATGG	GCTCCATTGT	CCAGCTCAGC	CAGTCTGTCA	660
CTGCCTATAT	GGTGTCTGCC	GCAGGGCTGG	GTCTGGTCGC	CATTACTTT	GCTACACAGG	720
TAGTATTGAA	CAAGAGCGAC	TTGGCCAAAT	ACTCAGCGTA	GAAAACCTCC	AGCACATTGG	780
GGTGGAGGGC	CTGCCTCACT	GGGTCCCAGC	TCCCCGCTCC	TGTTAGCCCC	ATGGGGCTGC	840
CGGGCTGGCC	GCCAGTTCT	GTTGCTGCCA	AAGTAATGTG	GCTCTCTGCT	GCCACCCCTGT	900
GCTGCTGAGG	TGCGTAGCTG	CACAGCTGGG	GGCTGGGGCG	TCCCTCTCCT	CTCTCCCCAG	960
TCTCTAGGGC	TGCCTGACTG	GAGGCCTTCC	AAGGGGGTTT	CAGTCTGGAC	TTATACAGGG	1020
AGGCCAGAAG	GGCTCCATGC	ACTGGAATGC	GGGACTCTGC	AGGTGGATTA	CCCAGGCTCA	1080
GGGTTAACAG	CTAGCCTCCT	AGTTGAGACA	CACCTAGAGA	AGGGTTTTG	GGAGCTGAAT	1140
AAACTCAGTC	ACCTGGTTTC	CCATCTCTAA	GCCCCTTAAC	CTGCAGCTTC	GTTAATGTA	1200
GCTCTTGCAT	GGGAGTTCT	AGGATGAAAC	ACTCCTCCAT	GGGATTGAA	CATATGAAAG	1260
TTATTGTAG	GGGAAGAGTC	CTGAGGGGCA	ACACACAAGA	ACCAGGTCCC	CTCAGCCCAC	1320

AGCACTGTCT	TTTGCTGAT	CCACCCCCCT	CTTACCTTTT	ATCAGGATGT	GGCCTGTTGG	1380
TCCTCTGTT	GCCATCACAG	AGACACAGGC	ATTAAATAT	TTAACCTATT	TATTTAACAA	1440
AGTAGAAGGG	AATCCATTGC	TAGCTTTCT	GTGTTGGTGT	CTAATATTC	GGTAGGGTGG	1500
GGGATCCCCA	ACAATCAGGT	CCCCTGAGAT	AGCTGGTCAT	TGGGCTGATC	ATTGCCAGAA	1560
TCTTCTTCTC	CTGGGGTCTG	GCCCCCAAA	ATGCCTAAC	CAGGACCTTG	GAAATTCTAC	1620
TCATCCAAA	TGATAATTCC	AAATGCTGTT	ACCCAAGGTT	AGGGTGTGTA	AGGAAGGTAG	1680
AGGGTGGGGC	TTCAGGTCTC	AACGGCTTCC	CTAACCAAC	CTCTTCTCTT	GGCCCAGCCT	1740
GGTTCCCCC	ACTTCCACTC	CCCTCTACTC	TCTCTAGGAC	TGGGCTGATG	AAGGCAGTGC	1800
CCAAAATTC	CCCTACCCCC	AACTTTCCCC	TACCCCCAAC	TTTCCCCACC	AGCTCCACAA	1860
CCCTGTTGG	AGCTACTGCA	GGACCAGAAG	CACAAAGTGC	GGTTTCCCAA	GCCTTGTCC	1920
ATCTCAGCCC	CCAGAGTATA	TCTGTGCTTG	GGGAATCTCA	CACAGAAACT	CAGGAGCACC	1980
CCCTGCCTGA	GCTAAGGGAG	GTCTTATCTC	TCAGGGGGGG	TTTAAGTGCC	GTTCGCAATA	2040
ATGTCGTCTT	ATTTTTAG	CGGGGTGAAT	ATTTTATACT	GTAAGTGAGC	AATCAGAGTA	2100
TAATGTTAT	GGTACAAAAA	TTAAAGGCTT	TCTTATATGT	TTA		2143

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGGGCTGTAC	CAGGGCGTGC	CCAGAGCTGA	GCCGGGCACC	GAGGCCCGGA	GACACTATGA	60
TGAAGGCAGTT	CGGATGGGCA	GCCTGGGGCT	GTTCCCTGCAG	TGCGCCATCT	CCCTGGTCTT	120
CTCTCTGGTC	ATGGACCGGC	TGGTGCAGCG	ATTCGGCACT	CGAGCAGTCT	ATTTGGCCAG	180
TGTGGCAGCT	TTCCCTGTGG	CTGCCGGTGC	CACATGCCTG	TCCCACAGTG	TGGCCGTGGT	240
GACAGCTTCA	GCCGCCCTCA	CCGGGTTCAC	CTTCTCAGCC	CTGCAGATCC	TGCCCTACAC	300
ACTGGCCTCC	CTCTACCACC	GGGAGAAGCA	GGTGTTCCTG	CCCAAATACC	GAGGGGACAC	360
TGGAGGTGCT	AGCAGTGAGG	ACAGCCTGAT	GACCAGCTTC	CTGCCAGGCC	CTAACGCTGG	420
AGCTCCCTTC	CCTAATGGAC	ACGTGGGTGC	TGGAGGGAGT	GGCCTGCTCC	CACCTCCACC	480
CGCGCTCTGC	GGGGCCTCTG	CCTGTGATGT	CTCCGTACGT	GTGGTGGTGG	GTGAGCCCAC	540
CGAGGCCAGG	GTGGTTCCGG	GCCGGGGCAT	CTGCCTGGAC	CTCGCCATCC	TGGATAGTGC	600
CTTCCTGCTG	TCCCAGGTGG	CCCCATCCCT	TTTATGGGC	TCCATTGTCC	AGCTCAGCCA	660
GTCTGTCACT	GCCTATATGG	TGTCTGCCGC	AGGCCTGGGT	CTGGTCGCCA	TTTACTTTGC	720
TACACAGGTA	GTATTGACA	AGAGCGACTT	GGCCAAATAC	TCAGCGTAGA	AAACTTCCAG	780
CACATTGGGG	TGGAGGGCCT	GCCTCACTGG	GTCCCAGCTC	CCCGCTCCTG	TTAGCCCCAT	840
GGGGCTGCCG	GGCTGGCCGC	CAGTTCTGT	TGCTGCCAAA	GTAATGTGGC	TCTCTGCTGC	900
CACCTGTGC	TGCTGAGGTG	CGTAGCTGCA	CAGCTGGGGG	CTGGGGCGTC	CCTCTCCTCT	960
CTCCCCAGTC	TCTAGGGCTG	CCTGACTGGA	GGCCTTCCAA	GGGGGTTTCA	GTCTGGACTT	1020
ATACAGGGAG	GCCAGAAGGG	CTCCATGCAC	TGGAATGCGG	GGACTCTGCA	GGTGGATTAC	1080
CCAGGCTCAG	GGTTAACAGC	TAGCCTCCTA	GTTGAGACAC	ACCTAGAGAA	GGGTTTTGG	1140
GAGCTGAATA	AACTCAGTCA	CCTGGTTTCC	CATCTCTAAG	CCCCTTAACC	TGCAGCTTCG	1200
TTTAATGTAG	CTCTTGATG	GGAGTTCTA	GGATGAAACA	CTCCTCCATG	GGATTGAAAC	1260
ATATGAAAGT	TATTGTTAGG	GGAAGAGTCC	TGAGGGGCAA	CACACAAGAA	CCAGGTCCCC	1320
TCAGCCCCACA	GCACGTCTT	TTTGCTGATC	CACCCCCCTC	TTACCTTTA	TCAGGATGTG	1380
GCCTGTTGGT	CCTTCTGTTG	CCATCACAGA	GACACAGGCA	TTTAAATATT	TAACCTATTT	1440
ATTTAACAAA	GTAGAAGGGA	ATCCATTGCT	AGCTTTCTG	TGTTGGTGTG	TAATATTTGG	1500
GTAGGGTGGG	GGATCCCCAA	CAATCAGGTC	CCCTGAGATA	GCTGGTCATT	GGGCTGATCA	1560
TTGCCAGAAAT	CTTCTTCTCC	TGGGGTCTGG	CCCCCCTAAA	TGCCTAACCC	AGGACCTTGG	1620
AAATTCTACT	CATCCCCAAAT	GATAATTCCA	AATGCTGTTA	CCCAAGGTTA	GGGTGTTGAA	1680
GGAAGGTAGA	GGGTGGGGCT	TCAGGTCTCA	ACGGCTTCCC	TAACCACCCC	TCTTCTCTTG	1740
GCCCAGCCTG	GTTCCCCCCTA	CTTCCACTCC	CCTCTACTCT	CTCTAGGACT	GGGCTGATGA	1800
AGGCACGTGCC	CAAAATTCTC	CCTACCCCCA	ACTTCCCT	ACCCCCAACT	TTCCCCACCA	1860
GCTCCACAAAC	CCTGTTGGA	GCTACTGCAG	GACCAGAAGC	ACAAAGTGC	GTTCCTCAAG	1920
CCTTGTCCA	TCTCAGCCCC	CAGAGTATAT	CTGTGCTTGG	GGAATCTCAC	ACAGAAACTC	1980
AGGAGCACCC	CCTGCCTGAG	CTAAGGGAGG	TCTTATCTCT	CAGGGGGGGT	TTAAGTGCCG	2040
TTTGCAATAA	TGTCGTCTT	TTTATTTAGC	GGGGTGAATA	TTTATACTG	TAAGTGAGCA	2100
ATCAGAGTAT	AATGTTTATG	GTGACAAAAAT	TAAAGGCTT	CTTATATGTT	TA	2152

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AGCTCGGAAT TCCGAGCTTG GATCCTCTAG AGCGGCCGCC GACTAGTGAG CTCGTCGACC
CGGAAATT

60
68

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

AATTAATTCC CGGGTCGACG AGCTCACTAG TCGGCGGCCG CTCTAGAGGA TCCAAGCTCG
GAATTCCG

60
68

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AGCGGATAAAC AATTCACAC AGGA

24

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TGTAAAACGA CGGCCAGT

18

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TGTTCCCTGCC CAAATACC

18

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GGTCTGGTCG CCATTTAC

18

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGGGCAACAC ACAAGAAC

18

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TCAGCCCCCA GAGTATATC

19

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GCTCCATGCA CTGGAAATG

18

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ACCCAGGACC TTGGAAAT

18

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ACACCCTAAC CTTGGGTAAC

20

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CCTAGAAACT CCCATGCAAG

20

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TGGCAGCAAC AGAAACTG

18

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ACTATCCAGG ATGGCGAG

18

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TGATTGCTCA CTTACAGT

18

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TGGTTAGGGA AGCCGTTG

18

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

AGCCCCAATGA CCAGCTAT

18

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

TTCCCAAATGC TGTTACCCAA GG

22

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGTGCTCCTG AGTTTCTGTG TGAG

24

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 255 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Gly	Leu	Tyr	Gln	Gly	Val	Pro	Arg	Ala	Glu	Pro	Gly	Thr	Glu	Ala	Arg
1				5					10					15	
Arg	His	Tyr	Asp	Glu	Gly	Val	Arg	Met	Gly	Ser	Leu	Gly	Leu	Phe	Leu
						20		25					30		
Gln	Cys	Ala	Ile	Ser	Leu	Val	Phe	Ser	Leu	Val	Met	Asp	Arg	Leu	Val
						35		40			45				

Gln Arg Phe Gly Thr Arg Ala Val Tyr Leu Ala Ser Val Ala Ala Phe
50 55 60
Pro Val Ala Ala Gly Ala Thr Cys Leu Ser His Ser Val Ala Val Val
65 70 75 80
Thr Ala Ser Ala Ala Leu Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile
85 90 95
Leu Pro Tyr Thr Leu Ala Ser Leu Tyr His Arg Glu Lys Gln Val Phe
100 105 110
Leu Pro Lys Tyr Arg Gly Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser
115 120 125
Leu Met Thr Ser Phe Leu Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro
130 135 140
Asn Gly His Val Gly Ala Gly Ser Gly Leu Leu Pro Pro Pro Pro
145 150 155 160
Ala Leu Cys Gly Ala Ser Ala Cys Asp Val Ser Val Arg Val Val Val
165 170 175
Gly Glu Pro Thr Glu Ala Arg Val Val Pro Gly Arg Gly Ile Cys Leu
180 185 190
Asp Leu Ala Ile Leu Asp Ser Ala Phe Leu Leu Ser Gln Val Ala Pro
195 200 205
Ser Leu Phe Met Gly Ser Ile Val Gln Leu Ser Gln Ser Val Thr Ala
210 215 220
Tyr Met Val Ser Ala Ala Gly Leu Gly Leu Val Ala Ile Tyr Phe Ala
225 230 235 240
Thr Gln Val Val Phe Asp Lys Ser Asp Leu Ala Lys Tyr Ser Ala
245 250 255

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly Asp Thr
1 5 10 15
Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu Pro Gly
20 25 30
Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val
35 40

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Arg Val Val Val Gly Glu Pro Thr Glu Ala Arg Val Val Pro Gly Arg
1 5 10 15
Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp Ser
20 25

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Gly Leu Tyr Gln Gly Val Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg
1 5 10 15
Arg His Tyr Asp Glu Gly Val Arg Met Gly Ser
20 25

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Asp Tyr Lys Asp Asp Asp Lys
1 5

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Met His Thr Glu His
1 5 10 15
His His His His
20